

GenCore version 5.1.3
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OM protein - protein search, using sw model
Run on: February 25, 2003, 16:05:26 ; Search time 93 Seconds

(without alignments);
697.902 Million cell updates/sec

Title: US-09-847-809a-3
Perfect score: 1701

Sequence: 1 MDLQFLMCUSLCATAFALK.....LFVGQSATDGEALYRHD E 315

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTRIMBL_21:
1: sp_archa:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebr:*

14: sp_uniclassified:*

15: sp_virus:*

16: sp_bacteria:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

RESULT 1
Q96RI3
ID Q96RI3
PRELIMINARY; PRT; 315 AA.

AC 096RI3;
DT 01-DEC-2001 (TREMBIrel. 19, Created)
DT 01-MAR-2002 (TREMBIrel. 20, Last sequence update)

DE Calumenin,

Homo_sapiens (Human); Chordata; Craniata; Vertebrata; Euteleostomi;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;

NCBI_TAXID=9606;

[1] InterPro: IPR002048; EF-hand.

RN Peterson R.E. Jr., Watson D.K.;

RT "Novel splice variant of human calumenin.";

RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL; ARF4563; AAC72908; 1; .

DR InterPro: IPR002048; EF-hand.

PFam: PF00036; efaend; 6.

DR PROSITE; PS00018; EF_HAND; UNKNOWN 4.

DR SQ SEQUENCE; 315 AA; 37335 MW; EIBF415B25076676 CRC64;

Query Match 93.1%; Score 1583; DB 4; Length 315;

Best Local Similarity 92.7%; Pred. No. 4.7-93;

Matches 292; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

1031.5 6 09M2A 09m2a6 sus scrofa

905 6 09n2A 09n2a6 bombyx mori

872.5 7 09r3A 09r3a6 mus musculus

859.5 8 09r3B 09r3b6 mus musculus

842.5 9 09r3C 09r3c6 homo sapien

804.5 10 09r3D 09r3d6 homo sapien

849.4 11 08S2K6 08s2k6 drosophila

77.9 12 023017 023017 caenorhabdi

742.5 13 09C0D4 09c0d4 mus musculus

579 14 070341 070341 mus musculus

564 15 09W0H8 09w0h8 drosophila

557.5 16 096051 096051 drosophila

17 483.5 28.4 342 5 09VMV2 09vmv2 drosophila
18 356.5 21.0 313 5 09TYSB 09tysb caenorhabdi
19 297.5 17.5 259 4 096AA1 096aa1 homo sapien
20 268.5 15.8 418 5 095T97 095t97 drosophila
21 257 15.1 391 10 09FNNO 09fnno arabidopsis
22 247 14.5 348 4 09NZP7 09nzp7 homo sapien
23 240 14.1 261 5 09VDY9 09vdy9 drosophila
24 235 13.9 320 5 01887 01887 caenorhabdi
25 232.5 13.7 343 5 09U460 09u460 plasmidium
26 227.5 13.4 343 5 025793 025793 plasmidium
27 222 13.1 98 11 063339 063339 rattois norv
28 221.5 13.0 345 10 09STP7 09stp7 arabidopsis
29 154 9.1 482 5 09TZ47 09tz47 plasmodium
30 150.5 9.1 567 5 09T424 09t424 arabidopsis
31 150.5 8.8 542 5 09NJD9 09njd9 onchocerca
32 146 8.6 165 5 096609 096609 dictyostelia
33 143 8.4 531 10 09ZSA2 09zsa2 arabidopsis
34 143 8.4 531 10 09ZSA2 09zsa2 plasmodium
35 143 8.4 519 10 09E127 09e127 arabidopsis
36 142.5 8.4 323 10 08RW12 08rw12 arabidopsis
37 142.5 8.4 521 10 09C6P3 09c6p3 arabidopsis
38 142 8.3 493 5 015872 015872 paramecium
39 141.5 8.3 553 10 080700 080700 arabidopsis
40 141 8.3 465 10 041793 041793 zea mays (m
41 140.5 8.3 453 10 09S9V0 09s9v0 arabidopsis
42 137 8.1 163 13 012996 012996 xenopus lae
43 137 8.1 481 5 018652 018652 paramecium
44 137 8.1 582 10 09SI07 09si07 nicotiana t
45 136 8.0 540 10 081390 081390

QY	181 HPEEYDYMMDIVQVETMEDIDKNADGFIDLEEVIGDMYSHDGNTDEPEVKTEREQFVER	240
Db	181 HPEEYDYMMDIVQVETMEDIDKNADGFIDLEEVIGDMYSHDGNTDEPEVKTEREQFVER	240
QY	241 ROKNRDGKMDKEETKDWLPSDYDHAEEARHLVYESDQNKGDKLTKEEVVKDYLFGVS	300
Db	241 ROKNRDGKMDKEETKDWLPSDYDHAEEARHLVYESDQNKGDKLTKEEVVKDYLFGVS	300
QY	301 QATDFGEALVRHDEF 315	
Db	301 QATDFGEALVRHDEF 315	
RESULT 2		
O35783	PRELIMINARY; PRT: 315 AA.	RN [1]
AC	035783; 035783;	RN
DT	01-JAN-1998 (TREMBlrel. 05, Last sequence update)	RP TISSUE=BRAIN;
DT	01-MAR-2002 (TREMBlrel. 20, Last annotation update)	RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRATN;
DE	CBP-50 protein.	RA Hsu M.J.; Yen C.H.; Tzeng M.C.;
OS	Rattus norvegicus (Rat).	RA "Crocalbin: a new calcium-binding protein that is also a binding protein for crototoxin, a neurotoxic phospholipase A2.";
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	DE FEBS Lett. 445:440-444(1999). [2]
OC	NCBI_TaxID=1016;	RA SEQUENCE FROM N.A.
RN	[1]	RA Rhee M.J., Tzeng M.C.;
RP	SEQUENCE FROM N.A.	RA Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=BRATN;	DR EMBL; AFS57659; AAM76141.1; .
RA	Hsu M.J.;	DR InterPro; IPR002048; EF-hand.
RL	Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.	DR Pfam; PF00036; efhand; 6.
RN	[2]	DR SMART; SM00054; EFh; 3.
RP	SEQUENCE FROM N.A.	DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=BRATN;	FT NON_TER 1 1
RX	MEDLINE=93107083; PubMed=8416973;	FT SEQUENCE 296 AA; 34990 MW; D011D029ADE2A0E CRC64;
RA	Osawa, M.; Muramatsu, T. i.	SQ
RI	Rebicucalbin: a novel endoplasmic reticulum resident calcium-binding protein with multiple EF-hand motifs and a carboxyl-terminal HDER sequence"; J. Biol. Chem.: 268:699-05(1993).	Query Match 87.7%; Score 1491; DB 4; Length 296; Best Local Similarity 92.6%; Pred. No. 3e-87; Matches 274; Conservative 9; Mismatches 13; Indels 0; Gaps 0; Gaps
RT	DR EMBL; AJ001929; CAA05100.1; .	
DR	InterPro; IPR002048; EF-hand.	
DR	Pfam; PF00036; efhand; 6.	
DR	SMART; SM00054; EFh; 2.	
DR	PROSITE; PS00018; EF_HAND; UNKNOWN_4.	
RT	SEQUENCE 315 AA; 36996 MW; 06B7FED579929E98 CRC64;	
RT	Best Local Similarity 88.6%; Pred. No. 8.3e-89; Matches 279; Conservative 19; Mismatches 17; Indels 0; Gaps 0; Gaps	
QY	1 MDLROFLMCLSLCPLAKSKPTEKKDRVHPEQLSKVHNDQAQFDYDDHDAFLGAEERKS 60	QY 20 KPTEKDRVHPEQLSKVHNDQAQFDYDDHDAFLGAEERKS 79
Db	1 MDLROFLMCLSLCPLAKSKPTEKKDRVHPEQLSKVHNDQAQFDYDDHDAFLGAEERKS 60	Db 1 KPTEKDRVHPEQLSKVHNDQAQFDYDDHDAFLGAEERKS 79
QY	61 FDQLTPEESEKBRIGKTVSKIDGKDGFVTVDKLWDWKFAQRKWIYEDVERQMGHDINE 120	QY 80 IDGQDFGVVNDLWKIAQKRWIYEDVERQMGHDNLNEGDLSWEEKYNTAXVLD 130
Db	61 FDQLTPEESEKBRIGKTVSKIDGKDGFVTVDKLWDWKFAQRKWIYEDVERQMGHDINE 120	Db 61 IDADKDFGVYEGELKSWIKHQKQVYDQENQWQEDMNGDLISWDEYRVNTGYTL 120
QY	121 DGLVSWEKRNATGYVLLDDPPDGNYKOMYRDRFRKHAQDKDGLIATKEEFATFL 180	QY 140 DPPDPDGNYKOMYRDRFRKHAQDKDGLIATKEEFATFLHPEEYDYMKTIVQVETMED 19
Db	121 DGLVSWEKRNATGYVLLDDPPDGNYKOMYRDRFRKHAQDKDGLIATKEEFATFL 180	Db 121 DPPDPDGNYKOMYRDRFRKHAQDKDGLIATKEEFATFLHPEEYDYMKTIVQVETMED 18
QY	181 HPEEYDYMMDIVQVETMEDIDKNADGFIDLEEVIGDMYSHDGNTDEPEVKTEREQFVER	QY 200 IDKNAQDFIDLEEVIGDMYSHDGNTDEPEVKTEREQFVERDKNKGDKMKEETKDWL 250
Db	181 HPEEYDYMMDIVQVETMEDIDKNADGFIDLEEVIGDMYSHDGNTDEPEVKTEREQFVER	Db 181 IDKNAQDFIDLEEVIGDMYSHDGNTDEPEVKTEREQFVERDKNKGDKMKEETKDWL 240
QY	241 ROKNRDGKMDKEETKDWLPSDYDHAEEARHLVYESDQNKGDKLTKEEVVKDYLFGVS	QY 260 PSDYDAEEARHLVYESDQNKGDKLTKEEVVKDYLFGVSQATDFGEALVRHDEF 315
Db	241 ROKNRDGKMDKEETKDWLPSDYDHAEEARHLVYESDQNKGDKLTKEEVVKDYLFGVS	Db 241 PSDYDAEEARHLVYESDQNKGDKLTKEEVVKDYLFGVSQATDFGEALVRHDEF 315
QY	301 QATDFGEALVRHDEF 315	RN [1]
Db	301 QATDFGEALVRHDEF 315	
QY	301 QATDFGEALVRHDEF 315	
Db	301 QATDFGEALVRHDEF 315	